



Ms. Delora Dillard, OIPE

FROM: Anne-Marie Corrigan, STIC
571-272-2501

Per your request, please find re-run of latest raw sequence listing (RSL) of 10/658355.
Total pages: 9, includes cover sheet.

Thank you.

Best Available Copy

STIC Biotechnology Systems Branch**RAW SEQUENCE LISTING**
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/658,355A
Source: FJO
Date Processed by STIC: 3/16/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efb/efs/downloads/documents.htm>) , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Best Available Copy

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

101658, 355A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was refiled in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

Best Available Copy



IFWO

RAW SEQUENCE LISTING

DATE: 03/16/2004

PATENT APPLICATION: US/10/658,355A

TIME: 07:58:57

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

3 <110> APPLICANT: Gantier, Rene
4 Guyon, Thierry
5 Hugo, Cruz Ramos
6 Vega, Manuel
7 Driittanti, Lila
9 <120> TITLE OF INVENTION: Rational Directed Protein Evolution Using Two Dimensional
10 Rational
11 Mutagenesis Scanning
13 <130> FILE REFERENCE: 38751-923
15 <140> CURRENT APPLICATION NUMBER: US/10/658,355A
16 <141> CURRENT FILING DATE: 2003-09-08
18 <150> PRIOR APPLICATION NUMBER: 60/457,063
19 <151> PRIOR FILING DATE: 2003-03-21
21 <150> PRIOR APPLICATION NUMBER: 60/410,258
22 <151> PRIOR FILING DATE: 2002-09-09
24 <160> NUMBER OF SEQ ID NOS: 501
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply
Corrected Diskette Needed

(pg. 1-6)

ERRORED SEQUENCES

7445 <210> SEQ ID NO: 182
7446 <211> LENGTH: 55
7447 <212> TYPE: DNA
7448 <213> ORGANISM: Artificial Sequence
7450 <220> FEATURE:
7451 <223> OTHER INFORMATION: EcoRI Forward Primer
7453 <400> SEQUENCE: 182
E--> 7454 gctgtatga tttattggat gttggaattc.cgtgatgcgg tattttctcc ttacg
7455 (55)
7457 <210> SEQ ID NO: 183
7458 <211> LENGTH: 55
7459 <212> TYPE: DNA
7460 <213> ORGANISM: Artificial Sequence
7462 <220> FEATURE:
7463 <223> OTHER INFORMATION: EcoRI Reverse Primer
7465 <400> SEQUENCE: 183
E--> 7466 cctaaggaga aaataccgca tcagggaatt ccaacatcca ataatcata caggc
7467 (55)
7469 <210> SEQ ID NO: 184
7470 <211> LENGTH: 35
7471 <212> TYPE: DNA
7472 <213> ORGANISM: Artificial Sequence

please see
item # 1
on error
summary
sheet.

55
insert
here

55
insert
here

BEST AVAILABLE COPY

RAW SEQUENCE LISTING

DATE: 03/16/2004

PATENT APPLICATION: US/10/658,355A

TIME: 07:58:58

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

Same
errors

7474 <220> FEATURE:
7475 <223> OTHER INFORMATION: Seq Clai Forward Primer
7477 <400> SEQUENCE: 184
E--> 7478 ctgattatca accgcggtac atatgattga catgc
7479 35
7481 <210> SEQ ID NO: 185
7482 <211> LENGTH: 31
7483 <212> TYPE: DNA
7484 <213> ORGANISM: Artificial Sequence
7486 <220> FEATURE:
7487 <223> OTHER INFORMATION: Seq Clai Reverse Primer
7489 <400> SEQUENCE: 185
E--> 7490 taccggataa taccgcgcca catagcagaa c
7491 31
7493 <210> SEQ ID NO: 186
7494 <211> LENGTH: 18
7495 <212> TYPE: DNA
7496 <213> ORGANISM: Artificial Sequence
7498 <220> FEATURE:
7499 <223> OTHER INFORMATION: Seq Forward Primer
7501 <400> SEQUENCE: 186
E--> 7502 cctgatgaag gaggaactc
7503 18
7505 <210> SEQ ID NO: 187
7506 <211> LENGTH: 18
7507 <212> TYPE: DNA
7508 <213> ORGANISM: Artificial Sequence
7510 <220> FEATURE:
7511 <223> OTHER INFORMATION: Seq Reverse Primer
7513 <400> SEQUENCE: 187
E--> 7514 ccaagcagca gatgagtc
7515 18
7517 <210> SEQ ID NO: 188
7518 <211> LENGTH: 31
7519 <212> TYPE: DNA
7520 <213> ORGANISM: Artificial Sequence
7522 <220> FEATURE:
7523 <223> OTHER INFORMATION: IFN alpha-2b 5' Primer
7525 <400> SEQUENCE: 188
E--> 7526 tctgtgcaa gtcaagctgc tctgtgggt-g
7527 31
7529 <210> SEQ ID NO: 189
7530 <211> LENGTH: 48
7531 <212> TYPE: DNA
7532 <213> ORGANISM: Artificial Sequence
7534 <220> FEATURE:
7535 <223> OTHER INFORMATION: IFN alpha-2b 3' Primer
7537 <400> SEQUENCE: 189
E--> 7538 gctctagatc attcattaat tottaaactt tcttgcaagt ttgttgac

BEST AVAILABLE COPY

RAW SEQUENCE LISTING

DATE: 03/16/2004

PATENT APPLICATION: US/10/658,355A

TIME: 07:58:58

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

Same errors

7539 48
7541 <210> SEQ ID NO: 190
7542 <211> LENGTH: 36
7543 <212> TYPE: DNA
7544 <213> ORGANISM: Artificial Sequence
7546 <220> FEATURE:
7547 <223> OTHER INFORMATION: IFN alpha-2b HindIII Primer
7549 <400> SEQUENCE: 190
E--> 7550 cccaggetta tggccttgac ctttgcctta ctggtg
7551 36
7553 <210> SEQ ID NO: 191
7554 <211> LENGTH: 48
7555 <212> TYPE: DNA
7556 <213> ORGANISM: Artificial Sequence
7558 <220> FEATURE:
7559 <223> OTHER INFORMATION: IFN alpha-2b XbaI Primer
7561 <400> SEQUENCE: 191
E--> 7562 gctctagatc attccttact tcttaaaactt tottgcaagt ttgttgac
7563 48
7565 <210> SEQ ID NO: 192
7566 <211> LENGTH: 80
7567 <212> TYPE: DNA
7568 <213> ORGANISM: Artificial Sequence
7570 <220> FEATURE:
7571 <223> OTHER INFORMATION: IFN alpha-2b 80 bp 5' Primer
7573 <400> SEQUENCE: 192
E--> 7574 cccaaggetta tggccttgac ctttgcctta ctggtggccc tcttggtgct cagctgcaag
E--> 7575 80
E--> 7576 tcaagctgct ctgtgggctg
7578 <210> SEQ ID NO: 193
7579 <211> LENGTH: 20
7580 <212> TYPE: DNA
7581 <213> ORGANISM: Artificial Sequence
7583 <220> FEATURE:
7584 <223> OTHER INFORMATION: EMCV Forward Primer
7586 <400> SEQUENCE: 193
E--> 7587 ccgtacatt gaggcaccca
7588 20
7590 <210> SEQ ID NO: 194
7591 <211> LENGTH: 21
7592 <212> TYPE: DNA
7593 <213> ORGANISM: Artificial Sequence
7595 <220> FEATURE:
7596 <223> OTHER INFORMATION: EMCV Reverse Primer
7598 <400> SEQUENCE: 194
E--> 7599 caggagcagg acaagggtcac t
7600 21
7602 <210> SEQ ID NO: 195
7603 <211> LENGTH: 22

BEST AVAILABLE COPY

RAW SEQUENCE LISTING

DATE: 03/16/2004

PATENT APPLICATION: US/10/658,355A

TIME: 07:58:58

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

*SAME
errors*

7604 <212> TYPE: DNA
7605 <213> ORGANISM: Artificial Sequence
7607 <220> FEATURE:
7608 <221> NAME/KEY: misc feature
7609 <222> LOCATION: 1; 22
7610 <223> OTHER INFORMATION: EMCV Probe: n at position 1 is a 5-carboxyfluorescein
7611 (FAM)-modified deoxycytidylate; n at position 22 is an N,N,N',N'-
7612 tetramethyl-6-carboxyrhodamine (TAMRA)-modified deoxythymidylate.
7614 <400> SEQUENCE: 195
E--> 7615 ~~naagctca~~ agacccaacc gc
7616 (22)
8074 <210> SEQ ID NO: 208
8075 <211> LENGTH: 41
8076 <212> TYPE: DNA
8077 <213> ORGANISM: Artificial Sequence
8079 <220> FEATURE:
8080 <223> OTHER INFORMATION: Oligonucleotide
8082 <400> SEQUENCE: 208
E--> 8083 ~~aaacatgtg~~ tgatctgect caaaccacac gcctgggtag c
8084 (41)
8086 <210> SEQ ID NO: 209
8087 <211> LENGTH: 46
8088 <212> TYPE: DNA
8089 <213> ORGANISM: Artificial Sequence
8091 <220> FEATURE:
8092 <223> OTHER INFORMATION: Oligonucleotide
8094 <400> SEQUENCE: 209
E--> 8095 ~~aaagatctc~~ attccttact tcttaaactt tcttgcaagt ttgttg
8096 (46)
8098 <210> SEQ ID NO: 210
8099 <211> LENGTH: 41
8100 <212> TYPE: DNA
8101 <213> ORGANISM: Artificial Sequence
8103 <220> FEATURE:
8104 <223> OTHER INFORMATION: Oligonucleotide
8106 <400> SEQUENCE: 210
E--> 8107 ~~aaacatgtg~~ tgatctgect caaaccacac gcctgggtag c
8108 (41)
8110 <210> SEQ ID NO: 211
8111 <211> LENGTH: 46
8112 <212> TYPE: DNA
8113 <213> ORGANISM: Artificial Sequence
8115 <220> FEATURE:
8116 <223> OTHER INFORMATION: Oligonucleotide
8118 <400> SEQUENCE: 211
E--> 8119 ~~aaagatctc~~ attccttact tcttaaactt tcttgcaagt ttgttg
8120 (46)
19072 <210> SEQ ID NO: 500
19073 <211> LENGTH: 46

BEST AVAILABLE COPY

RAW SEQUENCE LISTING

DATE: 03/16/2004

PATENT APPLICATION: US/10/658,355A

TIME: 07:58:59

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

19074 <212> TYPE: DNA
19075 <213> ORGANISM: Artificial Sequence
19077 <220> FEATURE:
19078 <223> OTHER INFORMATION: primer reverse INFA-E159H
19080 <400> SEQUENCE: 500
E--> 19081 aaggatcctc attccttact tcttaaactg tgttgcaagt ttgttg
19082 46
19084 <210> SEQ ID NO: 501
19085 <211> LENGTH: 46
19086 <212> TYPE: DNA
19087 <213> ORGANISM: Artificial Sequence
19089 <220> FEATURE:
19090 <223> OTHER INFORMATION: primer reverse INFA-E159Q
19092 <400> SEQUENCE: 501
E--> 19093 aaggatcctc attccttact tcttaaactc tgttgcaagt ttgttg
19094 46

Same errors

Best Available Copy

VERIFICATION SUMMARY

DATE: 03/16/2004

PATENT APPLICATION: US/10/658,355A

TIME: 07:59:00

Input Set : D:\923seq.002

Output Set: N:\CRF4\03162004\J658355A.raw

L:7454 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:182
L:7466 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:183
L:7478 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:184
L:7490 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:185
L:7502 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:186
L:7514 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:187
L:7526 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:188
L:7538 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:189
L:7550 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:190
L:7562 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:191
L:7574 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:192
M:254 Repeated in SeqNo=192
L:7587 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:193
L:7599 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:194
L:7615 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:195 after pos.:0
L:7615 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:195
L:8083 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:208
L:8095 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:209
L:8107 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:210
L:8119 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:211
L:19081 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:500
L:19093 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:501

BEST AVAILABLE COPY